

## SEQUENCE LISTING

<110> ASTRAZENECA AB

5 <120> GPR22

<130> NGAP/100041

<140>

10 <141>

<160> 2

<170> PatentIn Ver. 2.1

15

<210> 1

<211> 1881

<212> DNA

<213> Human

20

<400> 1

gttattttctt caaaaaggaaa acacaatttt cttttatatac aaaacaatgc aaacttgatg 60

gttcttaattt ctacattttc tattaaatgtt ttacaaaactt aaaaattaaa ctaagtacac 120

aattgaaaaga ttttttttc ttacaaagaa cacgttatac gtcattttaa ttgccaaata 180

tcaaaatagg tattcttattt cactttctag gggaaaaaac caactgctcc aaaagaatgt 240

gtttttctcc cattctggaa atcaacatgc agtctgaatc taacattaca gtgcgagatg 300

acattgatga catcaacacc aatatgtacc aaccactatc atatccgtta agctttcaag 360

tgtctctcac cggattttctt atgttagaaaa ttgtgttggg acttggcagc aacctcaactg 420

tattggtaact ttactgcattt aatatccact taatcaactc tgttagtaac attattacaa 480

30

tgaatcttca tgtacttgat gtaataatgg tttttttttt tttttttttt tttttttttt 540

tccttctgtt ttcactggag agtaacactg ctctcatttg ctgtttccat gaggcttgg 600

tatcttttgc aagtgtctca acagcaatca acgtttttgc tatcactttt gacagatatg 660

acatctctgtt aaaaacctgca aaccgaattt tgacaatggg cagagctgta atgttaatga 720

tatccattttt gatttttttt tttttttttt tcctgattcc tttttttttt gtaaaatttt 780

35

tcagtcttca aagtggaaat acctggaaa acaagacact tttatgtgtc agtacaaaatg 840

aataactacac tgaactggga atgttattatc acctgttagt acagatccca atattttttt 900

tcactgttgtt agtaatgtta atcacataca ccaaaaatact tcaggctctt aatattcgaa 960

taggcacaag attttcaaca gggcagaaga agaaagcaag aaagaaaaag acaatttctc 1020

taaccacaca acatgaggct acagacatgt cacaaggcag tgggggaga aatgttagtct 1080

40

ttgggttaag aacttcagtt tctgtataaa ttggccctccg gcgagctgtg aaacgacacc 1140

gtgaacgacg agaaagacaa aagagagtct tcaggatgtc tttattgatt atttctacat 1200

ttcttctctg ctggacacca atttctgtt taaataccac catttatgt ttaggcccaa 1260  
 gtgacctttt agtaaaatta agattgtgtt ttttagtcat ggcttatgga acaactata 1320  
 ttcaccctct attatatgca ttcactagac aaaaatttca aaaggcttg aaaaagtaaaa 1380  
 taaaaaagcg agttgttct atagtagaag ctgatcccct gcotaataat gctgtataac 1440  
 5 acaactcttg gatagatccc aaaaagaaaca aaaaaattac ctttgaagat agtgaataa 1500  
 gagaaaaaacg ttttagtgcct caggttgtca cagactagag aaaagtctca gtttcaccaa 1560  
 atccacatc aatgagttt taaaattttaa ttgtaaaaac tgatattact gccaaatata 1620  
 agaaaaatat tttaagtatt gtttatgtt taaatttca atgtgaatg ctaatttagat 1680  
 aggtcatata tattcaattt cttcattact taatgtat ttgcatggc agttgttaa 1740  
 10 agtactatca tgtgtatatt ttgtcaatat tatgtccaac agaaaatatt catgtaaagtc 1800  
 atattttta aggaataaat acatagcctt aaaacagtgt ataactttaa aatgtaaaaaa 1860  
 aaaaaaaaaa aaaaaaaaaa a 1881

15 <210> 2  
 <211> 433  
 <212> PRT  
 <213> Human

20 <400> 2  
 Met Cys Phe Ser Pro Ile Leu Glu Ile Asn Met Gln Ser Glu Ser Asn  
 1 5 10 15

25 Ile Thr Val Arg Asp Asp Ile Asp Asp Ile Asn Thr Asn Met Tyr Gln  
 20 25 30

Pro Leu Ser Tyr Pro Leu Ser Phe Gln Val Ser Leu Thr Gly Phe Leu  
 35 40 45

30 Met Leu Glu Ile Val Leu Gly Leu Gly Ser Asn Leu Thr Val Leu Val  
 50 55 60

Leu Tyr Cys Met Lys Ser Asn Leu Ile Asn Ser Val Ser Asn Ile Ile  
 65 70 75 80

35 Thr Met Asn Leu His Val Leu Asp Val Ile Ile Cys Val Gly Cys Ile  
 85 90 95

40 Pro Leu Thr Ile Val Ile Leu Leu Ser Leu Glu Ser Asn Thr Ala  
 100 105 110

Leu Ile Cys Cys Phe His Glu Ala Cys Val Ser Phe Ala Ser Val Ser  
115 120 125

Thr Ala Ile Asn Val Phe Ala Ile Thr Leu Asp Arg Tyr Asp Ile Ser  
5 130 135 140

Val Lys Pro Ala Asn Arg Ile Leu Thr Met Gly Arg Ala Val Met Leu  
145 150 155 160

10 Met Ile Ser Ile Trp Ile Phe Ser Phe Phe Ser Phe Leu Ile Pro Phe  
165 170 175

Ile Glu Val Asn Phe Phe Ser Leu Gln Ser Gly Asn Thr Trp Glu Asn  
180 185 190

Lys Thr Leu Leu Cys Val Ser Thr Asn Glu Tyr Tyr Thr Glu Leu Gly  
195 200 205

Met Tyr Tyr His Leu Leu Val Gln Ile Pro Ile Phe Phe Phe Thr Val  
210 215 220

Val Val Met Leu Ile Thr Tyr Thr Lys Ile Leu Gln Ala Leu Asn Ile  
225 230 235 240

Arg Ile Gly Thr Arg Phe Ser Thr Gly Gln Lys Lys Lys Ala Arg Lys  
245 250 255

Lys Lys Thr Ile Ser Leu Thr Thr Gln His Glu Ala Thr Asp Met Ser  
260 265 270

30 Gln Ser Ser Gly Gly Arg Asn Val Val Phe Gly Val Arg Thr Ser Val  
275 280 285

Ser Val Ile Ile Ala Leu Arg Arg Ala Val Lys Arg His Arg Glu Arg  
35 290 295 300

Arg Glu Arg Gln Lys Arg Val Phe Arg Met Ser Leu Leu Ile Ile Ser  
305 310 315 320

40 Thr Phe Leu Leu Cys Trp Thr Pro Ile Ser Val Leu Asn Thr Thr Ile  
325 330 335

Leu Cys Leu Gly Pro Ser Asp Leu Leu Val Lys Leu Arg Leu Cys Phe  
340 345 350

5 Leu Val Met Ala Tyr Gly Thr Thr Ile Phe His Pro Leu Leu Tyr Ala  
355 360 365

Phe Thr Arg Gln Lys Phe Gln Lys Val Leu Lys Ser Lys Met Lys Lys  
370 375 380

10 Arg Val Val Ser Ile Val Glu Ala Asp Pro Leu Pro Asn Asn Ala Val  
385 390 395 400

Ile His Asn Ser Trp Ile Asp Pro Lys Arg Asn Lys Ile Thr Phe  
405 410 415

Glu Asp Ser Glu Ile Arg Glu Lys Arg Leu Val Pro Gln Val Val Thr  
420 425 430

20 Asp